

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCCGCGCTGGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGCCAGGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAAACTTGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCAGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACTGAATGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTGCACCTGCAGAACG
TTGGCCGCCATGGCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGATTAAATTCCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRAALGLPLLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCGSGDGRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSIC~~T~~ACDESCKTCG~~L~~NRDCGECEVGWVLDE
GACVDVDECAAE~~PPP~~CSAAQFCKNANGSYTCEECDS~~S~~CVGCTGEGPGNC~~E~~CISGYAREHGQCADVDEC~~S~~LAEKT
CVRKNEN~~CY~~NTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGC**A**TGCCCGAGGAGCGCCTTC
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCCTGCGCTGGCACTGCAGGGCGGAGGC
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTACCAAGGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGCTTGAAAACAGGATGGGTGGCAGCATTGAAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT
TCTTAAAACATGTCAACAAGCTGAGTGCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCC
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACGCTCAACCACCTGCTTAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTATTTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCGAGCCTGGCTGTGGC
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATAACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAGGCCAGGGAGCGGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTGTTCAGTGCCTGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCTAAACATTACAATGCATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTAGATATTAGAT
GTTTGTACATTTAAAATTGCTCTAATTAACTCTCAATAACATATATTGACC
TTACCAATTCCAGAGATTCACTATTAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACCTTGCAT
TGGCTTGAAGCAATAATATATTGTAACAAAACACAGCTCTACCTAATAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGCCGGCGCAGCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCTGGCGTCCGGCGTCGCAGAGCCAGGAGGCCAGGAGGCCAGGAGGCCACCATGTGCGATGTCACACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGCTCGGCCAGCAGGGCTGCGGGCCGG
GAGCTAGCACCGGGCTGCACCTGCACCGGGCATCCGGACGCCAGGGCAGGCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCACTCGGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTCCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGAACGTACTGGACAACGTGAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCCTGGATGAGGGCATTGCTACGCCCTGGGACCA
TCCGCCATCTCCTCGGTATGAAACATGCATGAAATTATACTAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTTGA
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCCACAGCAGCTGTCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCCGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAAGGAGCTGATGGAGAAATGGCCCTGTCACGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGAAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGATCGTGCAGCGCGTCAATGAGTGCACATCGAG
AGCTTGTGCTGGCGTCTGGGCGCGTGGGATGGAGGACATGGGTATCACTGAGGCTG
CGGGCACACCGCGGGCTCGGCCCTGGGATCCAGGCTAAGGGCGGCCAGGGCGTAAT
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCGGCCAGGGCGCTAAT
CCCAGCGGGTCTGGCTGACGCAAGGCCCTGGGAGCCGGCAGGCAGGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGCTGGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAACTCCGTATTCTTTTTTTTTAGACAGGGTCTTGTCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGCACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACCT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTGCCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGAAGTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCATCCGCGCAGTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTGAACTGCGTGG**AT** GACTCACAGGACTACTACGTGGCAAGAAGAACATACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAAGTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCA**G****T****A** AGGCTGAGATGAAGTGGACTGAGTAGAACTGG
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGCTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFFHGPAGSTLNPLVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGAGCAGTCGAGTTGTGGCTCCGCCACCCGCCGACCAAGCGCACAC
GGCGGCCCAAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTGCGGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAA**AT**GGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT
GAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAACAAATTAAATATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTACAGGTTCTCCATTGCAGGAAAAC
AATATTGAGACCAATTTCACGGCTGCTTGCCCCAGCTTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAAGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATATTGTACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAAGAT
AAACACATTCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCTCACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG
GGATGGCGTCAGGGAATTAAATATGAATCTTGTCCCTGCCCACCACGGACCCCCGGCCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCCGACCAACTCAGCTCCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTTACACATCGAAACTTCCCACGATT
CTGACTGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGCATA
CAAACTCACATGGGTAAAATGGGCCACAGTTAGTAGGGGCATCGTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGTTAACTACCGCGCGGTAGAAGACACCATTGTTAGAGGC
CACCACCCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGTCTCAGCGTCTTGTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTTGATAAAATGTTACACAGATGCAT
TTGTCATTGAAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVLYGNQLDEFPMLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLNSNLQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDRGRERVTPPISERIQLSIHVFND
TSIQVSWLSQLFTVMAYKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCCGCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCAGGGCGAAGAGGCGCAGGAGGAAGACCCGGGTGGCTCGGCCCTCGCC
TCGCTTCCCAGGCAGGCCCTCGCAGCCTTGCCCTTGTGCTGCCCTTGAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCAGGGCAGGGCAGGGCGGTACGTGGAGGTCCATCT
CTAGGGGAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCTCTGTGAGAAACAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGAGGTTCATCGTGGACA
TCTTGCATTCTGGACATTGGTCTGTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCTGTCAAGAGGTGCGGCATCTGTCCACCG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGACAGATGGAGACTCAGGACTCCGTGGCGAGGGTGGCTGCTGA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTCCTGTGGCAATTCAAGCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACCTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCACTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGTAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCAAATGGAAAACCTGCAAGCGAGTGGACCACTGTGAC
ACGAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGAGGATTCTCGTGTGCAAGAGGCTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCTCTGCACTGTGCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAATGGACTCTTGCTCTGGGGGACACGGTTGTGAACATTGTGTGAAGCAGTGAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATAGTACTCCGTGAAGATGGAAAACCTGCAAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGTGTGAACAGTGCAGACTCATACAGTGCAGTGTGCTTGAGGGATTCCGGCTCG
CTGAGGATGGGAACACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACATGGCTGCCAACACATTGTGTTA
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGAGCGGAAGACGGTGCAGAAT
GCACTGAAGGCCAATTGACCTGGTTTGATGATGGATCCAAGAGTCTGGAGAAGAGAATTGGAGGTG
TGAAGCAGTTGTCACTGAAATTAGATTAGTCTGACAATTTCACCGTCAAGGCTGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACCTCAACTCAGCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAGGGCTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTAACTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGACCAGCCATTGTTCACCGACGGACGGGCTCAGGATG
ACGTCCTGGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CTGTTCTAATTTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT
CCCATTCAACAAACCTCAGGAAGGCCCTTGAAGAAAAACAGATCAATGCAAATGAAAACCTTATAATGT
TCCAGAACCTTGCACAGAACAGAAGTAAGAAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCAGCACATTGTTAGTCATTGTATCACGGATTACAAT
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACTAATTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAAATATACTGTGGACAC
AACTTGCTCTGCCCTACCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTAAATACAAATTAAACACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGHRARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMTGLAIQYALNIAFSEAE GARPLREN VPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFIAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYILREDGKTCRVDHCAQQDHGCEHICVNSDDSYTCECLEGFR LA
EDGKRCRKDVCKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGMGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEE DNL LRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGC
CATGATTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAACGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGCCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGCTTCTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGGTGTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCT
TTCCTCTGTCACCTCCGACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGACTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC
TTTACTGTGGAAAACCCTCACTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAACATGAAATATGTGTTTTCATTTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCVTLEVSTGPGAA
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKAIAPIRTPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPPTDGAHPQPISPPIPGGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGGGTTTTCCACTTG
TTGAATTGTCCTATACTCAAAATTGCAACAGACACCTGTCTCCAAATGAAAATGTGA
AATACGCAATGGAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAATGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTAAGGATATCCCAGAGCTTCC
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATA
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATA
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAAAATAACATTACATTAAGTCATGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT
ACCTCTGGTCTTCAGTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTATTGTTGGGTGTCATCTACAACAAAGGGATTTGCA
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTGGCACAAACCAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT
GGGGTCTCCATGTTGTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCAGGGATGTTCATTTTATTCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGCCCCGTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACGTACAAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAATTAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACTCGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTTGAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTTCACCATTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAANINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTLSNSTLTFVKTVNNFVQRDTFVVWDKLSVNRRTHLTLMHTVEQATLRISQSFKTTEFDTNSTDIALKVFDFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLSSSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAFWNYPDTMNGSWSSEGCELTYSNETHTSCRCHLTHFAILMSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGLHYFFLAFAFWMCIEGIHLYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSaalgyryygtTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNVPCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636, 648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181, 188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154, 155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329, 346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394, 434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGAATGTTGCAGTGATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCAGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGTCACCCCGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCGGGCCCCGGGAGGGGGCTGGGCTGGGCGGGAGGCAG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCGTGTGGACTGCCGCCGGG
CAGAGCGCCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG
CGTGCACAGCGTGCGGTACCTCTGCATGGGCCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCAGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTCCGCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAA
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCTCAGTTCTGCTGAATAACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGGAGCTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCCGTGTACCTGC
TTCCATCTCCCAGGCCACCAGCCCTTGCCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGAGCAGGGAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCTTACATTATTTATGCCCTAAATTATATTATGTATGTAAAGTGGAGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTCAGGGCCCCGGCCTCTGCCTGCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCCTCCTGCTG
CTGCTGCCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATAACACATGGTTAACCGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTG
TGTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCTTAGTGATTCCGTTGTGGCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAACAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATTG

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
LLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVI
SVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAAACATGCTCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTTATGGCATTCATCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAAATTATCTCAGTCACCAAT
ATTAATGTA~~AAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA~~
ACTGCCTGAAAAATGCTGTCGA~~ACTGAGCAACTTACAAGAACTCTATATTAAATCACAACT~~
TGCTTCTACAATTTCACCTGGAGC~~CTTATTGGCCTACATAATCTTCTCGACTTCATCTC~~
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAA~~TCAAGACATGAACTTTAACGCTCTTATCA~~
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAA~~ATACAGATAACGCCCTGGTT~~
GGACTGGAAA~~ACTTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT~~
TGCTCTTCAA~~AAAGTTGTAATCTCAAATTTCGATCTAAATAAAATCCTATTAAATAGAA~~
TACGAAGGGGTGATT~~TTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCCT~~
GAGCTGATT~~CCATCGATAGTCTGCTGTGGATAACCTGCCAGATTTAACGAAATAGAAGC~~
TACTAACACCC~~TAGATTGTCTTACATTCAACCCAAATGCATTTTACAGACTCCCCAAGCTGG~~
AATCACTCATGCTGAACAGCA~~ATGCTCTCAGTGCCCTGTACCATGGTACCATGGTAC~~
CCAAACCTCAAGGAA~~ATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTG~~
GATGAACATGAACAA~~ACACATTGGATTGAGGCCAGATTCACTGTTTGCCTGGACC~~
CACCTGAATT~~CCAAGGTCAGAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGT~~
CTCCCTCTTATAGCTCTGAGAG~~CTTCTTAATCTAAATGTTAGAGCTGGGAGCTATGT~~
TTCCTTCACTGTAGAG~~CTACTGCAGAACACCAGCCTGAAATCTACTGGATAACACCTTCTG~~
GTCAAA~~AAACTCTGCCTAATACCCGTACAGACAAGTTCTATGTCATTCTGAGGGAACACTA~~
GATAAA~~ATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT~~
TGGCGCTGACT~~TGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG~~
GCTCTTGAAT~~ATTAAAATAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA~~
AGTTCTAA~~AAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA~~
TGCTGCGCAA~~AGTGCCTGAATACCATCTGATGTCAGGTAATAATCTTACTCATCTGAATC~~
CATCAACTGAGTATAA~~AAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA~~
TGTGTAAT~~GTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAGAATAATAC~~
CACAA~~ACACTTATGGCCTGTCTGGAGGCCCTGGGGATTATTGGTGTGATATGTCTTATCA~~
GCTGCC~~CTCTCCAGAAATGAAC~~TGTGATGGGACACAGCTATGTGAGGAATTACTTACAG~~~~
AAACCAAC~~CTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAA~~
AGAAAAAAGTACATCA~~TGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT~~
~~AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC~~

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNAVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDNKNPINRIRRQDFSNMLHLKELGINNMPPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPFQGQNVHQVFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLIDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSAAQSARI PSDVKVYNLTHLPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTLLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACACATTGAA
ACTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTC SNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGATGCAGGTGAGCAAGAGGAATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTAACCGAGCACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCAACAACACTCTAACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGCC
CATCGTCTGGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCACTTGGACACCATTGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGGAGCTGGCGTGGTGGAGGCCCTATGCCTTCCGGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCTGCGACTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTCAACCGGCAGCAGGCCACGTGCGGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTACCTGCCGCC
CCCGCATCCGGACCGAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTCAGTT
GTGTGCCGGGCCATGGCGACCCGCCGCCCCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCGTATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGGCCCCATGCCAACAA
GACCTTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTCGACATCAAGACCCTCATCGCCACCACCATGGCTTATCTTT
CTGGCGTCCTCTCTGGCTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCGCCAGTTCAACATGAAGATGATATGAGGCCGGGGGGGGCAGGGACCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGCGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCC
CCAGCCCTACCACCTGCCCTCTTCTACCGACCTCAGAAGGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPI~~L~~LLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSI~~H~~CNLTA~~V~~PYLA~~V~~RHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTTLEESVFHSVG~~N~~LET~~L~~LD~~S~~NPLA
CDCRLLWVFR~~R~~RWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLP~~N~~YFTCRRARI~~R~~RKAQQV
FVDEGHTVQFVCRADGDP~~P~~PA~~I~~LWLSPRKHLVSAKSNGRLTVFP~~D~~GTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFC~~L~~VLLFLWSRGKGNTKH~~N~~IIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGCACCTCGGCCCCGGCTCCGAAGCGGCTCGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCAGCCGCTCGCTCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTACCTCACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAACTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCACGGAGAACCAACCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTGCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACGCTGTGCTACACTGTGAGGGTCGCGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTACAGTGGCACCTACGGCTGCACAGCCACCAAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGGACACGCCATCATCAATGCAGAAGGGC
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATAGAGGCGCTGCCACTTCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC
TTTGGGTGCGGTTTGTACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCCTGG
CTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGATTCTGTT
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCATGGCAATT
CCTCACTCGACTTTCCATAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGTAACAGGCTGAAAAGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCCCGCCCTG
CCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACCTTCAGAGGTTGGGTTAAAGATGAAC
GATCATGCCAACACCAGGGTCTGCTCAAACGGAGGTACAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCCCTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTTGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGGATCTGGCAACAAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCAGGA
GAAATTGCCGGGCTGCAAAACCTAGAGTACCTGAACAGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCGCACAGTAAAACAGCACTGGGTTGGGGAGACCGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCTCCGGACTGCTGCTGGT
GTTGTCACCTCCGCCCTCACCGTGGGGCATGCTCGTGTATTCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACCTCCCGCGTCCGAGATTAACTCCCTACAGACAGTCTGT
GAECTTCCCTACTGGCACAATGGGCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT
GACCCCTTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTGGCCCCGGGGCTGTGGGTTGGATGCCCGGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACCGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKICSCNEIEGDLHVDCEKKGFTSLQRFTA
P TSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNLHEIVPG AFLGLQLVKRLHINNNKIKSFRQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILILNDNLISTLPANV
FQYVPITHLDLRG
NRLKTL PYEEVLEQI PGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRV
VCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPPAQA
ET FAPGPLPTPKTNGQEDHATPGSAPNGGT
KIPGNWQIKIRPTAAIATGSSRNKPLANS
LPCPGCSDHI PGSGLK
KMNCNNRNVSSLADLK
P KLSNVQELFLRDNIHSIRKSHFVDYKNL
L LLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYN
AIQLILPGTFNAMPKLR
L I L L N N N L L R S L P V D V F A G V S L
SKLSLHN
NYFMYLPVAGVLDQLTSII
IQIDLHGNPWECS
CTIVPFKQWAERLGSEV
LMSDLKC
ETPVNFFRKDFM
LLSNDEICPQLYARIS
PTLTSHSKNSTG
LAETGTHSNSY
LDTSRVSISVL
VPGLL
LVFV
TSAFTVV
GMLV
FILR
NRKRS
KRRD
ANS
SASE
INS
LQT
VCD
SSY
WHNG
PYNA
DG
AHRVYDCGSHSLD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGAAGGCCAGCTGTAGAGGGCGGTGACC CGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCTTCGCCCTGTGCCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCG
CGCGAACACCCCCACTGCCGACCGTGCTGGCTCGGCCTCGGGGCTGCTACAGCCTGC
ACCA CGCTACCATGAAGCGGCAGGGCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGTCCGACTGGAGCGCAGGC GTTCCC ACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCTGGCTGTCTCCGACCCCGGGCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGTGAGGGCTGAGGCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCGCCGCCCCGG
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGAGG
CTTGCCTGCGAATGTGCTACGGCTTGCAGCTGGGAAGGACGGCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACGGGGTGCCTCAGGCGCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGT GATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC
CAGTTCTGCACATTGACAAAATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTTGCAGGGAGTCCCTTGGCTCTAGTGATGCATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACCGGGTAGTGCCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPAGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAAATTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCG
GGGGCGCGAACGCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTGCCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCAGAAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCACT
TTTATCAGACTTAAGTTAATGCAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACATACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGTCACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGATTAGCCGGCACTGTTATCACAACCATCACTCGCAGTGGAGTTG
CACGCCACAGTCTCGATCATCACATCTACAAAGAGGAAATTGGCAGTCAGCAGGCCGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCAGAACAGAGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG
TAAACAGTGAACTGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAGATCTATGTC
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT
GTTATTGTTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYPAVGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSENNELI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKT KNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTCTCCCCGCCTCAGCCCCATCCGTGTACATACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACCTTGGAG
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATAAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCGGACCTCTTC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGGAGAAGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGAT
ATCGCGGCCACCACCTGTAGGACCTCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQS PPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGTERPCGGYQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGP EESNCLQCKKGWALHHLKCVDIDE
CGTEGANCADQFCVNTEGSYECRDCAKACLGMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGF IKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCAGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT
GCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTACATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCGCTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGGCGTGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGGCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTGCAGGGGGC
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAAGTGGGTGCTGGAGCCCCCGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGCAAGGAGGCTCCAGCCATAGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGC**GATGGGGACAAA**
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCT
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATAACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGT**GAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT**
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCCCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGAGAGGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAGAGCAAAACTCCAGCTAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGAGGGACAGC**A**TGAGCGGCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCCAGGCCGCAGGCCAGCTCAG
GCTCGTGCCTACCCACCAAGTTCCAGTGCCGCACCAGTGGCTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGTGCACGGCCA
CCCAGACTGTCCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATTGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATTGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCA**A**CTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCC**T****G**AGGACAAGCAGTGGCCACCAACCGTCACTCACGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
-8
-9
-10

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCGDHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGCTCGGTATCTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGGCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTCACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCCGTACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTGCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTAGACAAATGAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPLICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASNDPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCTCCGCTCCGCCCTCCCCCGCTCCCGTGCCTGCAGTCGGTGGCTAGAGA
TGCTGCTGCCGGTTGCAGTTGCGCAGCCTCTGCCGCCAGCCGCTCACCGCCGT
AGCGCCGAGTGTCCGGGGCGCACCCGAGTCGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGCTGCGAGTCGGCTGCCGCCAGGGCTGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
ACAATTAGGAACTGGTATGTGGATGCCAGGACCTTATGCTGGACTGATGGCAGCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCTTGCACATATTCTGATGAGAAACCAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACACAGTTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCAC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTTCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGAAAATACACAGAAGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLLLV
VTTVVVCWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSCGEATPDDMCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGCTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCAGCAGGACACAAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTIFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTTGCAACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGACTCTTCTCCCCA
GTCCCAGAGGGTGTCA GGCTGGCTGACGCCCTGGCATTGCAAGGGACCGTGGAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGGTTGGCCGATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC CAGCACAGATTTGGGGTTTCAGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTCQTGWSLRAAKVVCRQLGCRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIVL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTCGGCTGCCTGGG
CGTCTCGGCCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCTACCTGCAGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTCAAGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCGTGCCAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGTGCCTTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACAGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGG**G****A****A****T****T****C****T****G****G****A****C****T****C****T****A**
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GA^TGA^TGC^TATG^AATTG^CCTAAACTAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCAGGTTCATAC^TTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTG^CACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACC^ACATGGCCATATTGTC^TACTGTGGCTCGGCAG
CTGGACATGTCTCGGTCCCCTCTTACTGGCTTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGA^ACTGGCTGCCTACAAATAACTGGAGTCAAACACATG
TCTGTGTC^TTAATTCGTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCA**A****A****G****C****A****C****T**AGTTCTGAAA^ACTGATT^ACCAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATT^ATAATGTTGA^ACTTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACC^ACTGTTCTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAA^AACCTT^AAGAGGTGACTTAAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTG^TGGCTCAC^TGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATA^TTTTATTGATTGACTTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATT^ACAATGAATATCATGA^ACTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATA^CCTCACATTCAATGCCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCA^TGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSIJVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGGACCGTGGCTGACTAGTTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGATGGTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTCCAGAAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAAGTGCATCCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACTGAGGATCAGCTTACTATGAAATTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTGAAGAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAAGTAACTGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGCCAAGTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTAGGGTCTGAAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAAATAATGGATGAAGCTATAA
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL
SLVGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWF
EAFFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDII
VAALTERSLMGMDWKGSQEYKKA
EKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWD
PYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
AAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCCCTGGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTCTCAGTGGCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCAGTTCAGCACCTTCACTCTGAGAACATCGTGAUTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAACAGGACAACAAGTCTCGTACCCG
CCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTTCACTCATACTGTGTCCTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTACCTGGCAAGCCTGGGACTCACTGGCCC
AGGCCTTAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCCTTCCATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGGCTAACCTCCAGTGGAGGGCCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTAACTATAG
ATTCACCTCTCAGCAAAGAGTCCCTTTGGAAAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTCTAGCTACTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTKNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESSLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCCGGGCCCCCGCTTAGAGAACACGCCATGACCA
CGTGGAGCCTCCGGGGAGGCCGGCCCGCACGGCTGGACTCCCTGCTGGCTTGGCTCTGGGCTTCCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGCTCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTTAACACCCCTCACCACTATGTTCCGTGAAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTGGAAACCTGGACCTGGAGGCCTTCGTCCTGATGGCCGAGAGATCG
GGCTGTTGGTATTCTGCGTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCTGGCATGAGGCTGAGGACAACCTAACAGGGCTTACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCAGGGTGGTCCACTTCAAGCGTGGGGACCTATGTCCTGCAAGTGGAGAATGAATATG
GTTCTATAATAAGACCCGCATACATGCCCTACGTCAAGAAGGGACTGGAGGACCGTGGCATTGTTGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCAGGGACTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCCAGGGACTCAGGCCAACATGGTGTGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTAACGCCATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCAACGGAGGCCAACATTGGCTTCAATGAG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCACTGACTATGATGTCAGGGACTCAGGCCAACATGG
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCCTGTGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCC
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCTCAGTGGCACGTGATGTCAGGGCAGG
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGTCAGGGCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGGAGTCACATGGGAGAATATTGATGACCAAGCGCAAAG
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAACATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAAGGTACCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTCACGGAAACCCCC
ACCTGGGAGGAACCAAGTACATTAAAGTGAGCGGTGGCACCCCTCTGCTGGTGCCTGGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCAACCCCTACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTAAACCTAACGGCTGCAGGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGGCGAGGCTGTGGCTCTAGGGTGGAGC
AGCTAATCAGATGCCACGCCCTTGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCGGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGCGTGCTCTTGCTGGTCTCTGGGAGGCTGGCCACATCCCTCATGGCCCC
TTTATCCCCGAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCCTCACACCTCTGAGCCTTCTTGGAAGGAACCTGGCTGAGAAACATGTGACTTCCCC
TCCCTCCCACTCGCTGCTCCACAGGGTGCAGGCTGGCTGGAGAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGCTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCAACATCC
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCAACATCCAGGG
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCAACATCCAGGGAGGAGG
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCAACAGCAGGGGAGAGCAGGCCCTCCTC
GAAGTGTGTCAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDW STLVPL RL RHQQL GLQAK GWN FM LED STFW
I FGGS I HYFR VP REYWR DR LLK MKAC GLN T LTYVP WNL HEP ERG KF DF SG NLD LEAF VL MA
AEIG LWV ILR PG PYIC SEM DLG GLP SW LL QD PGM RL RT TYKG FTEA VD LYFDH LMS RVV PLQ
YKR GGPI I AVQ VEN EYGS YN KDP AY MPYV KK AL ED RG IVE L L TS DN KDG LSK GIV QGV LAT
IN LQ STHE LQ LTT F L FN VQ GT QPK MVME YWT GW FD SW GG PHN I LD SSE VL KT VS AIV DAGS
S IN LYMF HG GT NF GFM NGAM HF HDY KSD VT SY DYDA VL TEA GDY TAK YM KLR DFF GSIS GIP
L PPPPD L L P KMPY EPL TP VLY LSL WD AL KYL GE PI KSE K P IN M EN LP VN NG NG QSF GYI LY
TS ITSS GIL SGH VHD RGQ VFVN TV S I GFL DYK TT KIA VPL I QGYTV LR I L VEN RGRV NYGEN
ID DQR KGL I GNL YL ND SP LKN FRI YSL DM KKS FF QRF GLD KWX SL PET PT LPA FFL G SLS IS
ST PC DT FLKLEG WE KG VVF ING QNL GRY WNI GP QK TL YL PGP WL SSG IN QVIV FEET MAG PA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTAGGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTACGGTCTGTCCCGCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**
AAGAACGCTGCTCGCTTCGTTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGGCC
CGTCCGCTATGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACCTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGCACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTCCCTGGACCTTACCTCCCCGAGCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGCCTGGCCGGCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCAATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGCTAACAGCAGTGAACAGGACCTTGTGAAGCCACCAATTCTG
GGCAAACAACTCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACT**GAAAGGTAGGCCGGCATGGTGGCTCATGC**
CTGTAATCCCAGCAGTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLLGRYWTQQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCGTCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTCCCTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCCCATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCTGGGTGTATTGCTCA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATACCCGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAACTAAGATAATATATGACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAACGGCTGATAGAACAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTAAGTCATTCAATTCAAATCATTGTTTTCTTTGGGG
AAAGGGAAGGAAAATTATAACTAAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA WVYLLK NLRELYLIGNLN SENN K MIGLES L REL RHL K ILHVKS NLT KVPSN
ITDVAPH LTKL VIHNDGT KLL VL NSL KK MMN VAE L EL QNCE LERI P HAIF SLS NL Q ELD LKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPS ITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP
EKVGQLSQLTQLELKGNCLDR LPAQLGQCRMLKKSGL VVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTTCCTCTGGACTTGCATTCCATTCTTTCATGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTTGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTATTATGCCTGTC
ATCGCTGGTGGTATCTGGCGGCTGCTCTGCTGATAGTTGCTGCTCTGCTTACTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAAGCTGTTGGCTGTAaaaATCACAAACCCAGACAAGGTGTGGTGGGCAAG
AACAGCCAGGCCAAAACCATTGCCACGGAGCTTGTCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA
AGTTTGATTCCCTGCCACCTGCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGGCACAGAAGAAAGGCCAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCAGGAAGGAGTTGGGAGAGAGAACCCACTGTTGGGAATGCTGATAAACCAGTCA
CACAGCTGCTCTTCTCACACAAATCTACCCCTGCGTGGCTGGAAC TGAGCTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCACATGGCAGAGACCCACAAGGCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTAAGGATGAAAACATTAAAGCTTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGCAGTAAAAGACTATGTCCTGATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAUTCAGCAAGAATTCAAAGAACTGTCCTTGCTTCTACTACTTCTCTCTAACATCTTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAAGGATCCTCACAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCAAATTGATTCTTGCATCTATGATGGCCCTCACCACCTGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTCACACCTCAATTATGCAGAAAACATCAACACTACATCTTAACTTGTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTAACTCTAATGGGAAATAACTTGTCAACTAAA
GACCCAATTGCGAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTTAAATGGATGTGGTACAATCAGA
AAGGTTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCTCCTCAACTTGTGATGTCACC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACAA
GAAGATGATGTAATACAAGTCAAATGCACTGGGAAATATAACACAGCATGGCTTTTGAAATCCAATTCA
TTTGGAAAAGACTATACTGAAATCACCATATTATGTTGGAACCAACTTTGTCTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATACCTGCTAGAGCCTCTCCACCTGACTTTGCATCTCCAAACC
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGATGAAACTTGTAAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTTGATATGTGAT
AGCAGTGGTACGTGAGCACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCCTGCATGAAAAAAA

FIGURE 70

MELVRRLMPLTLLILSCLAE LTMAEAE GNASCTVSLGGANMAETHKAMI LQLNPSENCTWTI
ER PENKSIRIIIFS YVQLDPGSCESENIVFDGTSSN GPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVVFYYFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDG PSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIIYITEDDVIQSQN ALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSR SKRDISSYKWKTDSIIGPIRLKDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCAGGGCAAGTCGGCATCTCATCCACTG
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCGCCCCAGCTCGTAGCGAGTGGTCTGGGGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTAAAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC
CTCTGGTGCCAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTGTGGAACGTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGGTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA
CATAAATGGAAAACGTGATGACAATAGACAAACTGTCTGGGCTATAGGAGGAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAACG
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCTACTACA
CACCTAATGTGTATGGTATAGACTGTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGAAAATAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTTCTTCTTCATTATAAAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGWSLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCCTGGCCAAGGCTTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTCAAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCCATAATTCAACACTCA
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACACTCGTGGCATCCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGCTGCGAGCTGGCTTGGAATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCGAGCTGGGAAATCAAAGGCCAAAGAACCAAGAAGAAAGTCCACCCCTT
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAACATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAAGTGC
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA
AGAGCAAAAGAATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATAACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCACTAATTGTTAAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATCCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCA
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTTATTTGCTGAGACTAATCTT
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AA YCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKA FPTNKNQQKEMIETKVVKEEKANDSNPNEESKKT DKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCATTGGATTGTGGAGTTCTTGCAA
TTGGCTAAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTCTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCTTCAAGGACTCTGCTTCAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGGAGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLVRKLPPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCCGGGTCACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCACTGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCCGGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCCCAGAGAAGGACGTGCTGGTGCCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGTGGCTTTCTTACCAAGTCCCCA
ACGGCGCTACCAGTTCAACTTCCACCGAGGGCCAGCAGGTCTGTGAGACAGCAGGCTGCGGTG
GTGGCCTCTTGAGCAGCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTTTGCCGCTGGAAAGTTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCTTAACGTGGGCCCCCAGAGCCTGGG
CCGAAGCTTGGCTCCCCGACCCGCAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCCTACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGCTGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCC
CAGCCTGGGGGAAGAAGAGGGCCTGGGGGCTCCGGAGCTGGCTTGGGCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGGAAATCTGAGGGAAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTGGCAA
AAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

MGLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**TG**ATGTGGCACCACAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCCCTGGACGGAAAGTGGCAAGGAATTGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCCAACCTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGGTGCGCTGGCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGCA
CATACGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCGCCCGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGGAGCTGACAGCCTTCCTGCACCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCAGCCTGGGAGGA
GGAGCCGGCGTGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGCTGAGCAA
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCT**TG**AGCACCACGACCTGCCACAGCCTAGAGGCCG
CACAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGCCAGGCCAGGAG
GCAGATGCAGTCCAGGCATCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCAACCCAGGGAGGGCTGTCATAGTCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAERAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGC GGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTCTGTCCTGTTCTTGTCGCTCCCAG
CCTGTCTGTCGTCTTGGCGCCCCCGCCTCCCCCGGGTGCAGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCCGAGGGCGCTCCCAGACCTAGAGGGGGCTGGCCTGGAGCAG
CGGGTCGTCTGTCCTCTCCCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGGGGCTCCCGCACCCCTGGCCTGCCGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCAACATGTCCGCAGCCTGGATCCCAGCTCGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCCCGGGAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTACACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCAGAGAAGAAAAC
CAATAAAGATTGTAAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTAAATTACAGAAGAATTGGGAAAGTGGCTCTAATGTTGGAAATTGGAAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCCAAGAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGGTATTATTGATGTTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACACATGCCCACTGGTTGGCACCAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCAGCCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTACAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTACTGATGAAATCAGATAACAAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCGCACCCGGGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGCGGGCTGCGGGCGCAGAGCGAG**ATGC**AGCGGCTTGGGCCACCCCTGCTGTGCCCTGC
TGCTGGCGGGCGGCGGCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTGAGGA**ACTG**TGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTA**CTGCCAGTTG**CCAGCTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCCAGGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT
GCACTGCTGGAGGGAAAGAGATT**TAG**ATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCAACCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCTTGTGCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCAT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGATTCTTGAGGCATGCACATCTGGAATTAA
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACTGGTTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCCAACACTGAACACTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACAGTTCTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCTCACTGAAGACTCACAGTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGGCTGGCATTACCTCTGCAGCTCCTTGCTGTGAGTCAAAAAACATGGGACGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGAGACGGAGGTGAGCAGATCAGTCACTTGAGGTCA
TTCGAGACCAGGGCTGGCCAACATGGAGAAACCCCCCATCTCTACTAAGGAAACATGGGAGGAGGAGGAGGAG
AGGTGCGCTGTAATCCCAGTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGACCGCTGCAGCTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACAAACACGGGAG
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTGATCCTCTTCTCCAGGGCTGCCCTGATGGGGCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GTGTAGAATGACTGCCCTGGGAGGGTGGCTTCTGGGCCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAA
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCCTGCCCCAGCTGAGCCTGACCTAGAGGAGAAC
ACTCTTGTAGCTGGGTTGGCTGGTGCCTGCACTGTGCCCCGGTGTACCCCTGGCATGTTCCCTGCC
GTGTGCGCTGCCAGATCCGGCCCTGGTATAACGCCCGCTGTCCTACCGCGAGGCTACCAACTGTGGACTG
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCTGAGAGCAACAGCATTG
CCGTGTGGACCAGAGTGAATGGCTACCTGGCCAATCTCACAGAGCTGGACCTGCCCCAGAACAGCTTT
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGAC
GGAGGACCACAGCTTGCAAGGGCTGGCAGGCTACAGGAACCTATCTAACCAACCAACCAGCT
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCATTG
CCGCTGGTTGAAATGCTGCCAACTGGAGACTCATGATTGGGGCAACAGGTAGATGCCATCTGGAC
GAACATTCCGGCCCTGGCAACCTGCGTAGCCTGGTAGCAGGATGAACCTGCCGGAGATCTCGACTATG
CCTGGAGGGGCTGCAAAGGCTGGAGAGCCTCCCTTCTATGACAACCAAGCTGCCGGG
GGAACAGGTGCCGGGCTCAAGTCTTAGACCTCAACAAGAACCCGCTCCAGGGGTAGGGCGGGGACTTGC
CAACATGCTGCACTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACA
GAACCTCCCCGAGCTGACCAAGCTGGACATCCAATAACCCACGGCTGTCCTCATCC
CCACCTGCCCAAGATGGAGACCCCTCATGCTCAACAAACGGCTCACTGGCCTTGAC
CCTGCCCAACCTGCAAGGGTAGGTTCTCACGGCAACCCATCCGGCTGTGACTGT
CACGGGCAACCGTGTCCGTTCATCGAGCCGAATCCACCCCTGTGCGGAGGCT
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACACTGTTGCCCTCATCT
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACT
GGTCACTCCAGGTGGCTTCGACTGACACCTGCCATGCAGGCA
GGAGCTGGAGGGTAGCAGCAGAACAGGGCAGGGCTATACACCTGT
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAG
GGTGCAGGAGACCCACCCCTATCACATCCTGTATCTGG
CTGGTCCAGTGCCCTCCCTCCGGGCCAGGGGCCACAGCT
CAACATTACCCGCTCTTCAGGCCACGGAGTACTGG
GTTGGCTTGTATGGGCCAGGACCAAGAGGGCACT
TGCCATCCTGGCTCTGCTGCTCTGCCAGCTGG
GGGTGTGGTGGAGGCGGCCCTCCAGCCTGGCTTCTGG
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGA
ACCATTGTCTAAAATTCTGAAAGCTCAGCCTGTTCT
AGAGAACATGGACCCACGTGCTGAGGGCTGGCAG
CAAGACAGATGGGCTTTGTGGCCCTGGGG
CTCTGCTGCCATTCTGAGGAACATCT
CCTCTGCCAGAGGCTCTGGCTGGCT
TCTTCTCTGTACAGTCTCAGTTGCTTGT
CTCGGGGGCTGCCCTCAATGTGGGAGTGAC
CGCCTCATCTCAGCAGCCTGGCTGGCATT
ATGTGTACACTCCCCAACCGATT
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSIHL
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMFRPLANLRSILVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMELMLNNNALSALHQQTVESLPNLQEVLHGPNIPR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDQLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGVADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATCGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGCCACACTCTTCAGATCCTGGCTCCTTCTACATCAGCCTAGTCATCTCTACGGCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGCTTCTGCGAGGTGAGTGAGAACAGCTGCGCAGCTGACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCCTACCAAGAACGCGCAGGACAAGCTGGAGCTGACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTCACCTGACGGGCAACCTGAGCGGAGAACACCGCTACATGTCATCGA
GGCCTTCTGCGCGAGAACCTGCGGGCGTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCTGAAAGACACTGGAGGAGCTGACCTGACGGGCAACCTGAGCGGAGAACACCGCTACATGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGTGGTCAAC
AGATGTGGCGTGCACCTGACAGCTGAGCTGAGCTGACCTCAACAAATGAGGGCACCAAGCTCATGCTCTAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
CCACAAACCTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCTAACGCTGTTACAACCACATGCCCTACATCCCCATCCAGATCGCAACCTCACC
CCTGGAGCGCCTCTACCTGAAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCGACATCGGCTCCTGCAAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGACCAACCTGACGCAAGATCGAGCTGGGG
CAACCGGCTGGAGTGCCTGCTGGAGCTGGCGAGTGCCTCAAGCGCAGCGCTTGGTGGAGGA
GGACCTGTTAACACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCCTGCCCAGTCAGGCCGGAGGGCAGGCCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGAGCCTGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGTCTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGAGGTCTGGACCCCTCACTTAGTTCTGGTATTATTTCTCCATCTCCACCTCTTCTCATCC
AGATAACTTATACTACATCCCAAGAAAGTTGACGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCTTCTTCCCC
TTGCTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGACTGTCAGGGCTGGCGAACCCAG
CCATGGGAGGGTCACCCAGCAGTGCCTGGCTCTGGCTCTGGCTGCCAGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGGCTGGAGCTGCTCTCAGTTTGTCAGGTTGGCAGTTAGTTAGTTTTGGTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGGATGGTTGGTATTAAAAGAAAAAAACCTAAAAAA
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTGTTGTTGGTTTTGGTGTCTTGTGTTCTTCTCC
ATGTGCTTGGCAGGCACTCATTCTGTGGCTGCGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCCGGATGAACGGTGCCTCATTGCACCTCCCTCCTGCGCTGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCAGACTTGTCTTCCCCACCTCCCTGCGCATGGGTGTG
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTCTCATGAAGAGCAGACACTTA
GAGGCTGGTGGAGGAAATGGGAGGTGCGCCCTGGAGGGCAGGCGTGGTCCAAGCCGGTCCCTGGCG
CTGGAGTGCACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTAGAGTCTTTGTCTTAATGATTATGT
CCATCCGTCTGTCGTCCTTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNEWTLDKLRQRITKNAQDKLELHLFMLSGIPDTVFSDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENRLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCAACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCAGGGACCATCAAGTGCAACTTGGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT
ACAGCATGTCCTTCAGAACAAAGGTCTGGCAGAGGTGTCAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACTAAAGCACTCCA
CGTCTACAATGGAGTCAGTCAGAATTCACACAGAGGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGTCTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCCCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCAGTGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAAC
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCGCAAGGACATCTTGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVAIIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPVRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGTGGCGACCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGCTGAGGCTGTGAGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCTAGAGAATGTGGCTGAGGCTGTGAGGCCATTCT
CACTGACCCACACGGTCAAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGTAACCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTTCGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCTGCAGTGGCTATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGAAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCAACTCCACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTGTAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCTGACATCCAGAAACAATGGCCTCAGTCATACTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTG
TCCATTGAGATTGCTCTCAGTTACTCATTGCCCCGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS
ELVQAVSDPSSPQYGYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEFLQWMLM
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTTCTC
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACCGCCTCCCTGTCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGGAAC
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTGCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGAGAATTCAACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTATTGCAACGTGGCTGTCAAAGGGGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAAGGGGG
TGACACAGTGTCCCTGGCAGCAATTAGGGTCTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCTTGCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTTGAAAACGT
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTGT
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV
LTAACIHDGKTYVKG
TQKLRVGFLKPDKFDGGRGANDSTS
AMPEQMFKQWIRVKRTHVPKGWI
GNANDIGMDYDYA
LLELKPKH
RKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR
ITPLKYAQICYW
IKGNYLDREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCATCTGCCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTTGGGGCCG
CCGGCGCTCCTAGGGCGCAGCGGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCTCGGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGCCCCGCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTATTAT
AGGTATTTGTAACCCTGCCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGGCCCAGGTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGTCCCCTGTCCCTGGCTACCACTGCAAGAACTCCCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCGTGTGGAAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCAAAGGG
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVCVGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAALSPLSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAE GPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCATTGGGAAGCCCCCTCAACAGAACCGGACTTAAGTCACAACAGATTATCTTCA
ACTTCTGTTCTCCCTCTGTTACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCA
CAAGGCAAGTCCATGAGGCACCTTCAAAGCCTCGAGAAGTGAACACTGAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGAAACTTTGACCTTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAAATGTTAGATGGACTGACATTCCAAGGCTTGG
TGCTCTGAAAGTCTGAAAGAAATGGAGTAAAGCAAACCTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGAGCTGGACCATAACAAACCTAACAGAGATACCAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTTCAACTTACAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTAACTAAC
ACTGCACATTGGAAACAACAGACTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAA
GCATTAAATACATCAAGCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCT
TCAGAGCTTGTAAATGCAGTTGCCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGCTGTTAGCCCAGA
TGGCTTGTGTTGATGATTCCAAACCCAGATCACGGTTAGCCAGAACACAGTCGGCAATAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTCGGCTGCGCAGGTGGAATTGCCAGTGAGGGAAATACAGTGTGTCATCTCAATCATTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTTCAGCAAATGC
AACTCTGACTGCTCTAGAAACACCATCATTGCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCATTGGTGGT
AACCGAGAGGCACTTTTGTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGGAGAACCTGGCCTCAGTGATGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACGCCACTCGTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGC
CGTGGTTGCTGTGGGGCACGTCAGCTGCTGGGTGATCATATACACACAAAGGGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAAAGCCACCAACAGTTGTCATCTCAGGTGCTGG
ATTTTCTTACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA
TCCTTGTAAACATATCATACAGGTTGCACTGACCCAGAACAGTTAATGGACCAACTGAGCCAGTT
CATAAAGAAAAAGGAGTGCCTACCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAATGGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC
TTATGACTTGGACACATGAGACTGAATGAGACCAAGGAAAAGCTTAACATACACTCAAGTGAACCTTATT
AAAGAGAGAAATCTTATGTTAAATGGAGTTATGAAATTAAAGGATAAAATGTTTATTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAATTAAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACTTGTGTTATGAAAAAAAGTATCTACGTAATTAAATGATATAACATGATTATTATGTT
TTATAATGCCAGATTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGTCACCATT
TTAAATAGAAGTACTTCATTATATTGACATTATTAATAAAATGTGTCATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSIKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQQLHLNTSSLLCDCQLKWLQPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVTER
HFFAAGNQLLIIVSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPS LDDDG
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPS YLSSQGTTLAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTAGACCCCGGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTACAAGAAAAAGTATGTTCTTTC
TATAAAGGAGAAAGTGAAGCCAAGGAGATATTTGGAAATGAAAGTTGGGCTTTTAGTAAAGTAAGAAGACT
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGGAGGAAATTAAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAGTGAACCGGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCACAGCAGTTGGA
TTTGTGCCCTATGTTGACTAAAATGACGGATAATTGCACTTCTTCATCAACCTCCTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCCTTCTCTTCTTAAACCACTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGAAACACAGATAAAATTATGAAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC
GCTGGCTCTCAACTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTCGTGGAGGTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTTGAGGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTTGGA
ACTCTTGACAATCGTCTACTACCATTCCGAATGGAGCTTTGTATACTTGCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACTCCTCTTGCCTCGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATGAGCTGGATCTCTGGGAATCA
TTTATCTGCCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAAACGGAATGCCCTTGACAACCTTCAGTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACACCCCTGGAAACTG
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCTCCGGT
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTCAGAACAGCTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGT
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGCTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATACAGGCTACACATGTATGGTGGTAA
TTCGGTTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTCTCTTCTTACTTTTCA
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGTGAGGGCACGGACCACAGATAACAAATGTGGGTCCCACCTC
AGTGGTCAGTGGAGACCAATGTGACCACTCTCAGACAGGACACAGGACAAAGTCAGAGAGAAAACCTT
CACCATCCCAGTGAATGATATAAACAGTGGATCCCAGGAATTGATGAGGTATGAAGACTACAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCTTCAAGATGAGGAAGCAGCACCA
TCGGAAAACCATCACGCCAACAGGACTGTTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATGAGCATGAGCACCTAAATCACTATAACTCATCAAATCTCCCTT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTGCTAGTGCATGAAACCGTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAATCAAAAAAA
GACAGTTATTAACATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTTATTCAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQI IKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNVGN
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTCGGTTCCCTCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCCGCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAGTTGTGCCCCGGCCCGAGCGCGCGCCGGCTGGAGCTTCGGTAGA
GACCTAGGCGCTGGACCGCGATGAGCGCGCCAGCCTCCGTGCGCGCCGGCTGGAGCTTCGGTAGC
GCGGTGCTGGGGCGCTGGCCGGTCCGACAGCGGGTGCAGGGAACTCGGGCAGCCTCTGGGTAGCGCC
GAGCGCCCAGCCCCACTACCTGCGCGTGCCTCGGGGACCTGCTGGACTTCAGTCAGTCAGGGCTAGCGCT
CCCGAGCCACTCCCCTCGGGTGCCTCGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTCC
ATGAGCCACCTCAAAGCTTCGAGAACAGTGAACAACATAAGGAGACCAATTCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCCTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACATTGGACCTTAGCAGCAACATATTTCAGAGCTCAAACAGTCATTTCCAGGCCACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTCAGCAATTGGGAAACACA
CTCCTGTGTTAAAGCTGAAACAGGAACCGAACACTCAGCTATCCCACCCAAGATGTTAAACTGCCCCACTGCAA
CATCTCGAATTGAAACCGAACAGATTAAAATGTAGATGGACTGACATTCCAAGGCTTGGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAAATTG
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATACACTGCACATTGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAGGCAGCTGATAACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATAGACCTGAGT
GACAACGCAATCATGTTTACAAGGCAATGCAATTTCACAAATGAAGAACATGCAACAATTGCAATTAAATACA
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACATTTCAGAGCTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCAGATGGCTTGTGTT
GATGATTTCACCAACCCAGATCACGGTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGGCTTCCAAATGACTTTGCTGGAAAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGGAAAATTATGCAACACCTCCGGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCTCGGCTG
CGCAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCCTTGGTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCCAAGAACGCCCCATGGATCTCACCACCGAGCTGGGCC
ATGGCACGCTGGAGTGCTGCTGCTGGGCCACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGATGCTGATGCCAGGGATGAGTCTTATGTTGAGTGAAGATA
GAGGACATTGGGTATACAGCTGACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTCGCGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGAGTGTAGCCATTGGTGGTAACCGAGAGGCAC
TTTTTGAGCAGGCAATCAGCTCTGATTATGTGGAACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGCTAAACACCTTGGACTGAGAGAGGAAACGTGCCCTCAGTGTGATCCCCACTCCAACCTGCACTCCCT
CAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGGTTGCTGT
GTGGGGCACGTCACTCGTGTGGGTGCTCATCATACACACAAGGGAGGAATGAAGGATGAGCATTAC
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATGTCATCTCAGGGAACGTTAGCTGACAGGAG
GATGGGTACGTTGCTTCAGAAAGTGGAAAGCCACCAAGTTGTACATCTCAGGTGCTGGATTTCCTTACCA
CAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAAGCTGATGTTGAAGCTGCCACAGATCTGTC
CTTTGTCGTTTTGGGATCCACAGGCCATTGTTAGGGAAATGTGTATGGCTCAGATCCTTGAACAA
TATCATACAGGTTGCACTCTGACCCAAGAACAGTTTAATGGACCAACTATGAGCCAGTTACATAAAGAAAAG
GAGTGTACCCATGTTCTCATCTTCAAGAACAGTTTAATGTCAGTAAATATGTCAGTGGCTTACAT
GTGAGGAAGCTTAACACTAGTTACTCTCAGAACAGTGAAGGACCTGGAAATGAAAAATCTGTTGCTAAACAAGTCC
TCTTGTGTTTGTGCAATCCAGAGCCAGCGTGGCTCGAGTAATTCTTCTGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTAT
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCAAGAGGAAGATGGGAAAGAACAGATTTTCA
GAAAATCACATTGTACCTTAAACAGACTTAAACAGACTTACAGGACTCCAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATTAAAGAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAAATTTTATACGGGAATGATGCTCATATAAGAACATACTTAAACTATTTTAAACTT
TTTATGCAAAAAGTATCTACGTTAAATTAAATGATATAACATGATTATTATGTTATTTATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT
ACTCATTATATTGACATTATATAAAATGTGCAATTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIGHNNRVSIAIDCAFRLSSLKTLDLKNNIEIS
WTIEDMNGAFSGLDKLRRRIILQGNRIRSITKKAFTGILDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLCDCQLKWLPQVAAENNQSFVNASCAPQQLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMPLSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPILLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLODDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSQQTLADRO
DGYVSSESGSHHQFVTTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTGACTGAATGGAAGGGCCGAGGCCGCGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCTGTGGGGCGCCCTGGCGCCGGGGCGCAGCAGGGAAAGGGGAAGCTGTTCTGCC
CTGCTCCACGAGGCCACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCCTATCCCTCCCTATATA
GAAACCTTCCACACTGGGAAGGCAGGGCAGGGCAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTACAGATTTACAGATACCAATGGAAGGGCAGGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGGCGACTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGTGTGCG
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGCCCCAGGATTGGCGAA
GTGGCGCCACAGCTGAGGCCGAAGAGAACGAATTGCGGAGGAGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGGCTGGCCAGCCCGGTAGCTGCCCGAGACTGTGCCGTGCTCCAGGAGGGCTGTTGACTGTG
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCCGTGAGCACACCAACCACCTATCTTGAGAACACAACCAGC
TGGAAAAGATCTACCCCTGAGGGAGCTCTCCGGCTGCACCCTGGAGACACTGAACCTGCAAAACACCCTG
CTTCCCGAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCAAAACAAGC
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGACTTGTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCAGAACAGCAAACCTGAGGTCTGTTGACCTGCACAAACAAGCTGGCAGACGCCGGG
TGGCGGACAACATGTTCAACGGCTCCAGCAACGCTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGGACTGAGCACCCCTGGGAGCTATACTGCAGAACAAACTACCTGACTGAGCAGGGCTGGCACACGAGA
CCTCTGGAAGCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACTGTCTGGTCCAGCTGGCTG
CGCGCAGCCTGGTGTGCTGCCTGGAGAACAGGCCATCGGAGCGTGGAGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCACAGCAACCAAGCTGCCAGGGCATCCACCCACTGGCTTCCAGGG
TCAAGCGGTTGCACACGGTGCACCTGTACAACAAACGCGCTGGAGCGCGTGCCTGGAGTGGCTCAGTGC
GCACCCCTCATGATCTGCACACCAAGATCACAGGCATTGGCGGAAGACTTGTGCCACCAACTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGGGTGCACCGCGACGCCCTCGCAAGCTGCCCTG
GCTCGCTGGACCTGTGGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCAGAGGGCGTGGCGGGATGGCTCAGCTGCCAGCTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCAGGCCCTGGGCCCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCCTGGTCCCCGCCATGCCACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGACAGTGCTTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGACATTCCAAGGACCGTGGCCCTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC
AGCACACGCCGTGTGCTGTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACCGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCAGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGGCCACACAAACTACCCCTCCAAACCCACCAAGCTCTGTCA
CCCCACTACCGCTGCCAGCCCTGTGAAATCATGCAGGGAGGGCTGCCCTGGCCATGCCACACAGGCCACCA
TCCCCTCCCCCTGTGACATGTGATGCGTATGCAACACACACACACATGCACAAAGTCATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGTGCCAGGCCAGAACATGCCATAGCAGCTGCCGTG
GTCCCATCTGTCCGTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGCCAGGTGCTGCCACCC
GGAACTCACAAAAGCTGGTTTATTCTTCCCATCCTATGGGAAGGAGGCCCTCAGGACTGCTGCCCTGGCC
TGGCCACCCCTGCTCCCTCCAGGTGCTGGCAGTCACCTGTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGGAAGGCCAGTGGAGGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACACCTT
GTTCTCAGGCTGTGGGGAAAGTTCCGGGTGCCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAA
CTCAAAGCTGATTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGAAAAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHTLNLYLANNK
LTLaPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQPQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAxFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCCCGCGCAGCAGACTGCTCCGGCGCGCCTGCCGCTGCTCTCCGGAGCGGCAG
CAGTAGCCGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCCTCCCATGGCGCCACCACCC
CAACCTGTTCTCGCGGCCACTCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTCTGGCGCTGGT
GCTGGGTATCTCGCTTAACCTGCAGGGCGCCGAGTCGACGGAGGTGGCCAGGAAATAGTGTATCGAT
TGGCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTGGGACAGTGTAGGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGCCAAACAAGTGCAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGCCCTGTAAGGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTACTGTCACCGATATACTGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACTG
CTCCATGGCAAACGTCACTGCTGATGGCTGTGATGTTAAGGACAAATACGGTGCCAGTGCCATCCCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGAGTGTGATGAATGTGCTCACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGCAACACTTGGGAGCTACATCTGCAAGTGTGATGCTAAAGGCTCGATCTCATGTATATTGGAGG
CAAATATCAATGTGATGACATAGACGAATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGCTCGATGTTATAA
CGTACGTGGCTCTACAAGTGCACGAAATGTAAGAAGGATACCAAGGTGATGGACTGACTTGTGTTATCCCCAA
AGTTATGATTGAAACCTCAGGTCCAATTGTCAGGAAAGGGAAATGGTACCATTTAAAGGGTACACAGGAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGCTCGAAGACACCATATATTCCCTATCATTACCAA
CAGGCCACTTCTAACGCAAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACCA
CCTGCCAACAGAGCTCAGAACACCTTACCAACCTACACCCCCAGAAAGGCCAACACCAGGACTGACA
ACTGACGAGCTAACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGG
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCAAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCGCCTCATGCATTAGGGACCTGTGCTGTGATTAGGCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGCAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCAATTGATGGTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCCATTGTTAGAATACTCATAAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTAAAAAATTAGA
AAAAAATTGTCATTTAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCCC
AGATGTTTGATCCTACTAGTAGTATGCACTGAAAATTCTTAGAACTAAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTTGTGACCTCTAAATGGAGAGGGATTGAAAGGGGAAGGCCAACATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAGGAAACTATTATCCAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTCAAGATTCTTAAAGAGATCCTCAAGGAACACAGTTCAGAGAG
ATTTTCATGGGTGCATTCTCTGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC
ACACCGGCAGACCTTCCCTCACCTCATCAGTATGATTAGCTTCTCTTCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTTGTCAATTAAACCTGTTAAAGGCAGGGCTGG
AGGGGGAAAATAATCTTAAGCCTTGTGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCA
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTACTTTACTTTGATGCC
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAATGTTT
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAAACAATTATGAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASSTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPA GGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTCCCTTGCAAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC
AACACAAGTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCCT
CTGGGGCTGTGGAGTATGTGGGAAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGAGGAACCCCTGTCAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGAAAATCATTGTCACCTTCAAGTATAACTGGAAATATCACTATTGATT
ATATCCATGTGTCTCTCTCTATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAGTGAACTTCTATGG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATTCTTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEIDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTGCAGTCCCCGGCAGTCCTGGTGTGTT
GCTTGCGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCGTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTGGTCCAGGTTCTGTTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAAATCTAGTTAAATTATAG
TTATCTTAATATTATGATTTGATAAAACAGAACAGATTGATCATTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCACTGCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG
GTTAAATAGTCTCTAATTTGAAAAATCGTGCCAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTAGAGAAAATATTCTCATTTGATATAATTCTCTG
TTCACTGTGAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGATTTCACTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTTGT
ATTTTTAGTTATGCAACTAAACTACCTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGTGATTC
CAACAAAGTTGATTCTCTGTATTTCTTACTATGGTTACATTTTATT
CAAATTGGATGATAATTCTGGAACATTTTATGTTTAGAAACAGTATTTTTTGTT
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAAATT
TTGGCCACTTTTCAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTGTTGTGATGTGAAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTCTTGATATGTCTAAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATATTAAAGACAA
ACTTCATATTATCCTGTGTTCTTCTGACTGGTAATATTGTGTTGGATTCACAGGTAAA
GTCAGTAGGATGGAACATTTAGTGTATTCTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAAACAAATGAATCAACTGACCATTACGTAGAC
AATTCTGTAATGTCCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATAACAGTTCTTAAAGCCCTCCTTAGAATTAAATATTGTACCATT
AAAGAGTTGGATGTGTAATTGTGATGCCTTAGAAAATATCCTAAGCACAAATAACCT
TTCTAACCACTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACATAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGGCGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGACACTTCCTCTGTGACCATTGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGGCGAATTCTCACCTTATTG
GGCACATGACTGACCTGATTATGCAAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCGTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGGATG
GGCCGCTCGGCCTACAATGAAAGGGACTATTATCATACTGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGGCTACCCGCCCTGCTC
TCCCTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGGTACTTGTAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGACTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGGG
GAGGGTGTCAAACACTGACACCCGTAGACAGAACAGGCTTTCTGTAGGTACCATGGCAA
CAGGGCCCCACAGCTGCTCATGGCTTCAAAGAGGAGGACGGAGTGGGACAGCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTGCACGAGCCACCGTGTGATCCAAGACAGGAGTCTCACTGTGCCAGCTA
CCGGGTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC
GTGGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTTGACAGCGG
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAACAGGAGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACGTTGACTTGACATCCTTCTGTCTCCCTCCTGGTC
CTTCAGCCCATGTCAACGTGACAGAACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTCAAGGCTGTGACAGGAGTACCTCAGGTGTT
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATGTCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIWSA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEPLPGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTTSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPsheraggNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCAATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGTCTGGAAAGCCAGCGGGCCTTGCTCTGTCTTGGCCTCATTGACCC
CAGGTCTCTGTTAAAACGAAAGCTACTACTGGCCTGGTCCCCATCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATTCGGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCCTGGGGTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCAGGCTGTAGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTGGCCGCTGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGGCCCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTACACACACTTGGGGCCACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCAGGCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTGGGGCCAGAGGAGTTCAATTG
GCGCAGCGAGCAGGGCCGTACTGTCACTGGGCTTGGCTACCTGTCACGGAGTCTCTGCTCGTGC
GGCACATCTGGATGGCTGGCAGGGAGACATTCTCAGTGGCCGTCTGACGAGTGGCTGGACGCTGCCTCATGG
ACTCTCTGGGCGTCGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACATGGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTGCCGTGACCCCTGTCCTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTCACCGCTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACACTCTGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTTCTCTGTGCAAGATGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGTATCGGGCCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTGGAAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA
GGGTAGCCTGCTGGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGTTCTCGAGGGCTTGCAGCCAATGTCC
TGGAGCCACGAGAACATGCTTACCCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGAGTTAGAGCAGGGTACCCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCACTCATGGACGTGGCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCACAGAGATCACCCCCAGGGCCCC
GGCAGGGCTTCTCCAGTCCATITCCAGGAGTTCAATCCTGCCCTGTCAACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTCTGGGGCTGCTTACACGCTGACTACCTGGCGCCGAGCCCGTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATTTCTCCGGTTCTCAGGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGTGGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCCTAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGCCAATAGCACTTAGCCCCTGGGGCCCTAACCTTACCTTCTGCTGCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRCG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLVVYGPREGGRGAPPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AACATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAACTG
GTTCTCCTTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAAT
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTCTAATACGTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGTAAAAAT

FIGURE 120

MLSSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYLKFLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCCGCTGCCGTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCAGGCCACCGCGAC
TCCGGCTCTGCCCTGCCGCTGACTTCTTCCTGCTGCTGCTTTCAAGGGCTGCCGTATAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGGAACTGTCTTGACATTAACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCAGGATGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGGACCCCTGCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCTTCCACTTAAACTCTGAAACAGGACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCAATTGCTTCCAATGACGCAGGCTCAGGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATGGCGAATTATTGGGGGGTTCTGGTGTCTTGTACTGGCCCTGA
TCACGTTGGCATCTGCTGTGCATAACAGACGGCTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACATCACATCCGCACTGACGAGGGAGGCCACTCAGACACAAGTCATGTTG
TGATCTGAGACCCGGGTGAGAGCGCACAGAGCGCACGTGCACTACATCTGCTGCTAGAAACTCCTGTC
GGCAGCGAGAGCTGATGCACTGGCACAGAGCTAGACACTCATTCAAGGCTTCTGTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAGGCCACATGAATAGAAATTTCCTCAAGATGGACCCGGTAAATATAACCA
GGAAGCGAAACTGGTGGCTTCACTGAGTTGGCTCTAATCTGTTCTGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACAGCCGTGCTGGAGATGGCGAGGTGGCTGGACAGCACCAGCGC
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCGCATTCCGGGGAAACCCA
GAAAAGGCTTCTACACAGCAGCCTTACTTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCACTGCTTCAATTGGAGAAGCTTTGGATCAGCATTTGTTAAACAAACAAAAATCAGGAAG
GTAAATTGGTGTGAGGGATCTTGCCTGAGGAACCCCTGCTGCTTCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAAATTT
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGTAAAGGTTCAACTTAAGGTAGAAGTCTAACGACTAGTGTAAAT
TGGAAAATATCAATAATTAGGTATTGGTACCCAAGGAATCCTCTATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTAGCCTTTCAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA
GCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGGTGGCCAGGCGCCCCGCTCTAGCTCACTGTCCTGCTGCTGCCAGGAGGCC
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCACTGCTGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTTCCATGCTAGCGTCCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGGTTAAATTGGAT
AAGATTGCTAAGGCAAAGGCAATTGCAAATCAACTGTCAAGTACAATAACATTGGAT
CCCAGTGTCTCTTGCACAGAGAAAGCACCAGGCCACAGGCTCTGCTGCTGCTGCTGCT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTGGTCTTCAAGAGCAGGTGTTCTCAGCCT
TGTGGGGGACATTAGCAACATCACTCAGAACCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCC
GAATGGCTCTCAACTCACCTGTCTTCAGCTTCAAGTGTCTGGGTTTTTAACTTGTGACAGCTTTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGAGGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCTGATGGCATCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCCTGGGATTACGCTCCAGCCT
TCTTGGTTGTCAAGTGTAGGGTAGCCTTATTGCCCCCTTCTTCTTAAACCTTACACTAGTGC
TGGGAAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGATTGGTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFFFRLRGCLIGAVNLKSSNRTPVVQEFESVELSCI ITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267